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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Application of:
Steven E. Cwirla et al.

Serial No.: 09/620,091 Group Art Unit: 1634

Filing Date: July 20, 2000 Examiner: Bradley L. SISSON

Title: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATION FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED USES

TRANSMITTAL LETTER

Director, Technology Center 1600
Crystal Mall 1
1911 South Clark Street
Arlington, VA 22202

Sir:

Transmitted herewith for filing is:

☒ Petition to Review Propriety of Restriction Requirement under 37 C.F.R. §1.144

☒ Return Postcard.

No fee is believed to be due with the filing of this Petition. However, should a fee be determined to be due, please charge the appropriate fees to Deposit Account No. 18-0580. **A duplicate copy of this sheet is enclosed.**

Respectfully submitted,

By: Shelley P. Eberle
Shelley P. Eberle
Registration No. 31,411

REED & ASSOCIATES
800 Menlo Avenue, Suite 210
Menlo Park, California 94025
(650) 330-0900 Telephone
(650) 330-0980 Facsimile

11/12/2002 CDESSAU 00000001 180580 09620091

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Title: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED USES

PETITION TO REVIEW PROPRIETY OF RESTRICTION REQUIREMENT UNDER 37 C.F.R. §1.144

Director, Technology Center 1600
Crystal Mall 1
1911 South Clark Street
Arlington, VA 22202

Sir:

This Petition Under 37 CFR §1.144 is in response to the finality of the Restriction Requirement.

A Restriction Requirement was mailed on October 2, 2001. Applicants mailed a timely and proper response on November 2, 2001, in which Applicants elected an invention with traverse under 37 CFR §1.143.

An Office Action was mailed on March 28, 2002, indicating that Applicants' traversal was not found to be persuasive and the requirement was deemed to have been proper and was made final.

Therefore, since Applicants made their election with traverse, they preserved their right to petition the finality of the Examiner's decision. Further, since the restriction requirement was made final, this Petition is timely filed.

THE FACTS

The Claims

Claims 1-17, 23-36, 42-54, 60-68, 74-94, 101-118, 124-141, 147-156 of the above-identified patent application are directed to compounds that bind to the granulocyte-colony

stimulating factor receptor (G-CSFR), and to pharmaceutical compositions containing such compounds..

Claims 18-22, 37-41, 55-59, 69-73, 95-100, 119-123, 142-146, 157-161 are directed to methods of treatment using compounds that bind to G-CSFR.

A complete set of the claims, as filed, are appended hereto as Exhibit A. While subsequent claim amendments were made, they bear no relevance to the properness of the restriction requirement and, therefore, are not presented here. For purposes of illustration, Claim 74 is set forth below, as it exemplifies the way in which the polypeptide compounds were recited:

> 74. A compound comprising a peptide chain approximately 12 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (V)
>
> (V) $CX^{IV}_1X^{IV}_2X^{IV}_3X^{IV}_4X^{IV}_5X^{IV}_6X^{IV}_7X^{IV}_8X^{IV}_9X^{IV}_{10}C$ (SEQ ID NO: 5)
>
> wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^{IV}_1 is E, G, P, N, R, T, W, S, L, H, A, Q or Y; X^{IV}_2 is S, T, E, A, D, G, W, P, L, N, V, Y, R or M; X^{IV}_3 is R, Y, V, Q, E, T, L, P, S, K, M, A or W; X^{IV}_4 is L, M, G, F, W, R, S, V, P, A, D, C or T; X^{IV}_5 is V, T, A, R, S, L, W, C, I, E, P, H, F, D or Q; X^{IV}_6 is E, Y, G, T, Q, M, S, N, A or P; X^{IV}_7 is C, V, D, G, L, W, E, V, I, S, M or A; X^{IV}_8 is S, Y, A, W, P, V, L, Q, G, K, F, I, E or D; X^{IV}_9 is R, W, M, D, H, V, G, A, Q, L, S, E or Y; X^{IV}_{10} is M, L, I, S, V, P, W, F, T, Y, R, or Q.

The Restriction Requirement

A Restriction Requirement was mailed on October 2, 2001. The Examiner required restriction to one of the following inventions:

I. Claims 1-16, 23-35, 42-53, 60-67, 74-93, 101-117, 124-140 and 147-155, drawn to a peptide compounds (classified in class 530, subclass 328); and Claims 17, 36, 54, 68, 94, 118, 141 and 156, drawn to a pharmaceutical composition comprising the peptide (classified in class 514, subclass 2).

II. Claims 18-22, 37-41, 55-59, 69-73, 95-99, 119-123, 142-146 and 157-161, drawn to a method of treatment (classified in class 514, subclass 2).

Applicants wish to note that Claim 100, directed to a method should have been grouped with Group II instead of with Group I.

The Examiner further required restriction as to the individual sequences identified in Groups I and II, asserting the position that each sequence was patentably distinct because they were unrelated sequences. Therefore, the Examiner required election as to Groups I or II, as well as an election as to a single sequence, citing M.P.E.P. 803.04.

Applicants' Response To Restriction

Applicants mailed a timely and proper response on November 2, 2001, in which Applicants elected the invention of Group I and further elected the polypeptide defined by SEQ ID NO:208, with traverse under 37 CFR §1.143.

Applicants did not traverse the restriction as to the inventions defined in Group I and II. Rather, Applicants traversed the restriction as to the election of a specific polypeptide, asserting that the election of a specific polypeptide was more properly an election of species.

Applicants asserted that all of the claimed polypeptides were functionally related because they were all G-CSF modulators. Furthermore, Applicants asserted that most of the claimed polypeptides (i.e., the polypeptides of SEQ ID NOS:8-432, 490 and 491) were also structurally related as encompassed by one of seven generic sequences. See Claims 1, 23, 42, 60, 74, 101, and 124, appended hereto. That is, seven generic sequences were provided that encompass all of the claimed polypeptides except for those set forth in Claim 147. Thus, examining all claims as one group, with the possible exception of claims 147 and claims depending therefrom, should be a relatively straightforward matter since a search need only be directed to each of the generic sequences of SEQ ID NOS:1, 2, 3, 4, 5, 6, and 7 provided in Claims 1, 23, 42, 60, 74, 101, and 124, respectively.

The Examiner has relied upon M.P.E.P. 803.04 to support his position of further restricting the invention as to individual polypeptides. In Applicants' response, the Examiner's attention was respectfully directed to M.P.E.P. 803, where it is states that "[i]f a search and examination of an entire application can be made without serious burden, the examiner must examine it on the merits . . ." [emphasis added]. This is true even though an application may include claims to distinct or independent inventions.

In respect to M.P.E.P 803.04, relied upon by the Examiner, although the section states that individual sequences are "presumed to represent an independent and distinct invention," this section also states that in order to:

> "aid the biotechnology industry in protecting its intellectual property without creating an undue burden on the Office, the Commissioner has decided *sua sponte* to partially wave the requirements of 37 C.F.R. §1.141 *et seq.* and permit a reasonable number of such nucleotide sequences to be claimed in a single application. It has been determined that normally ten sequences constitute a reasonable number for examination purposes. Accordingly, in most cases up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction."

Although this section of the M.P.E.P. is directed to nucleotide sequences, Applicants assumed that the Examiner's reliance on this particular section in the context of Applicants' polypeptide sequences was by way of analogy.

Thus, Applicants asserted that they were entitled to examination of ten sequences, examination of the seven sequences set forth in SEQ ID NOS:1-7 was appropriate and respectfully requested. For all the foregoing reasons, then, Applicants requested that the Examiner reconsider and withdraw the stated restriction requirement. In the event that the Examiner decided that some restriction requirement was still necessary, Applicants suggested an eight-way restriction requirement between SEQ ID NOS:1-7, and the polypeptides of Claim 147. The generic sequences clearly demonstrate the relatedness of individual sequences within any one generic sequence. In particular, five out of nine amino acids are conserved in generic SEQ ID NO:2, three out of six amino acids are conserved in generic SEQ ID NO:3, and five out nine amino acids are conserved in generic SEQ ID NO:4. If the restriction requirement were to be modified in this manner, Applicants indicated that they would then elect the polypeptides defined by SEQ ID NO:5 (claim 74), and, as the ten specific sequences that applicants are entitled to have examined, the ten polypeptides of SEQ ID NOS:184, 185, 208-213, 323, and 338.

The Finality Of The Restriction Requirement

A first Office Action on the merits was mailed on March 28, 2002 in which the Examiner indicated that the restriction was still deemed to be proper and was therefore made final.

APPLICANTS REQUEST RECONSIDERATION OF THE RESTRICTION REQUIREMENT

Applicants Assert That All Sequences Are Related And Are Properly Examiner Together

As noted above, all of the claimed polypeptides are functionally related because they are all G-CSF modulators. Furthermore, most of the claimed polypeptides are also structurally related as encompassed by one of seven generic sequences, i.e., seven generic sequences are recited that encompass all of the claimed polypeptides except for those set forth in Claim 147. Thus, examining all of the claims as one group, with the possible exception of Claims 147 and claims depending therefrom, should be a relatively straightforward matter since a search need only be directed to each of the generic sequences of SEQ ID NOS:1, 2, 3, 4, 5, 6, and 7 as recited in Claims 1, 23, 42, 60, 74, 101, and 124, respectively.

Applicants Assert That Reliance On M.P.E.P. 803.04 Is Misplaced

M.P.E.P. 803.04 indicates that nucleotide sequences encoding different proteins are structurally distinct chemical compounds and are unrelated to one another. These sequences are thus determined to normally constitute independent and distinct inventions.

There is no discussion in this section with regard to amino acid sequences, such as those that describe the polypeptides of the instant invention.

Applicants assert that the polypeptides of the instant invention are more properly considered under M.P.E.P. 803.02, which is directed to Markush-type claims. That section indicates that it is improper for the Office to refuse to examine that which Applicants regards as their invention, unless the subject matter in a claim lacks unity of invention. This section goes on to state that: "Broadly, unity of invention exists where compounds included within a Markush group (1) share a common utility, and (2) share a substantial structural feature disclosed as being essential to that utility".

Applicants assert that this unity of invention has been met. Using Claim 74 as an example, the recited polypeptide compounds share a common utility in that the polypeptide compounds are recited as all binding to the granulocyte-colony stimulating factor receptor (G-CSFR). In addition, the recited polypeptide compounds share a substantial structural feature in that they all comprise a peptide backbone with specifically recited variations therein. The backbone contains the generic sequences of SEQ ID NO:5:

(V) $CX^{IV}_1X^{IV}_2X^{IV}_3X^{IV}_4X^{IV}_5X^{IV}_6X^{IV}_7X^{IV}_8X^{IV}_9X^{IV}_{10}C$ (SEQ ID NO:5)

where each of the X^{IV} substituents is selected from a specific group of amino acids residues: X^{IV}_1 is E, G, P, N, R, T, W, S, L, H, A, Q or Y; X^{IV}_2 is S, T, E, A, D, G, W, P, L, N, V, Y, R or M; X^{IV}_3 is R, Y, V, Q, E, T, L, P, S, K, M, A or W; X^{IV}_4 is L, M, G, F, W, R, S, V, P, A, D, C or T; X^{IV}_5 is V, T, A, R, S, L, W, C, I, E, P, H, F, D or Q; X^{IV}_6 is E, Y, G, T, Q, M, S, N, A or P; X^{IV}_7 is C, V, D, G, L, W, E, V, I, S, M or A; X^{IV}_8 is S, Y, A, W, P, V, L, Q, G, K, F, I, E or D; X^{IV}_9 is R, W, M, D, H, V, G, A, Q, L, S, E or Y; X^{IV}_{10} is M, L, I, S, V, P, W, F, T, Y, R, or Q.

RELIEF REQUESTED

Applicants are not traversing the restriction as to Groups I (polypeptides and compositions) and II (methods of treatment).

Primary Request For Relief

Applicants hereby request that the examination of the seven sequences set forth in SEQ ID NOS:1-7 is appropriate and respectfully requested.

First Alternate Request For Relief

In the alternative, should the Examiner maintain the position that some restriction requirement is still necessary, Applicants hereby request an eight-way restriction requirement between SEQ ID NOS:1-7, and the polypeptides of Claim 147 and further request that such sequences be treated as Markush-type claims.

If the restriction requirement were to be modified in this manner, Applicants would then elect the polypeptides defined by SEQ ID NO:5 (claim 74). Further, should a polypeptide species election be required, Applicants would elect the polypeptide species having SEQ ID NO:208. If no prior art is found that anticipates or renders obvious this species, then it is understood that the Examiner will extend the search of the Markush-type claim. However, pursuant to M.P.E.P. 803.02, the prior art search will not be extended unnecessarily to cover all non-elected species.

Second Alternate Request For Relief

In the alternative, should the Examiner maintain the position that some restriction requirement was still necessary, Applicants hereby request an eight-way restriction requirement between SEQ ID NOS:1-7, and the polypeptides of Claim 147.

If the restriction requirement were to be modified in this manner, Applicants would then elect the polypeptides defined by SEQ ID NO:5 (claim 74), and, as the ten specific sequences that Applicants are entitled to have examined, the ten specific polypeptides of SEQ ID NOS:184, 185, 208-213, 323, and 338.

SUMMARY

This Petition is submitted for the purpose of removing the restriction requirement as between the individual polypeptide sequences, **or** by modifying the restriction requirement to be an eight-way restriction requirement between SEQ ID NOS:1-7, and the polypeptides of Claim 147, treating such sequences as Markush-type claims and possible requiring a single species election, **or** by modifying the restriction requirement to be an eight-way restriction requirement between SEQ ID NOS:1-7, and the polypeptides of Claim 147 and examining ten specific polypeptide sequences.

The appropriate fee accompanies this Petition. However, if for any reason any additional fees should be due, the Commissioner is hereby authorized to charge any fees to Deposit Account No. 18-0580.

If in the opinion of the reviewer, a telephone conference would expedite resolution of this matter, the reviewer is invited to call the undersigned at (650) 330-4916.

Respectfully submitted,

By: Shelley P. Eberle
Shelley P. Eberle
Registration No. 31,411

REED & ASSOCIATES
800 Menlo Avenue, Suite 210
Menlo Park, California 94025
(650) 330-0900 Telephone
(650) 330-0980 Facsimile

Exhibit A Complete set of the claims, as filed.

1. A compound comprising a peptide chain approximately 10 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (I)

(I) $CX_1X_2X_3X_4X_5X_6X_7X_8C$ (SEQ ID NO: 1)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X_1 is A, N, S, F, D, G, L, T, E, V, P, Q, H, M or K; X_2 is M, G, R, H, D, I, V, A, S, E, N, F, Y, P, C, W or T; X_3 is E, V, W, F, M, A, N, S, L, T, Y, G or P; X_4 is V, I, G, Q, W, M, T, Y, L, P, D, C, E or A; X_5 is M, E, W, L, P, N, I, T, V, F, Y, Q, S, R, W, G, H or D; X_6 is H, A, W, Y, V, F, Q, M, N, E, S, D, P or G; X_7 is M, F, Y, V, N, L, H, D, S, W, G, Q, C or T; and X_8 is C, Y, R, I, K, W, L, E, M, H, A, T, F, D, P, G or Q.

2. The compound of claim 1, wherein X_1 is D or P.
3. The compound of claim 1, wherein X_2 is D or P.
4. The compound of claim 1, wherein X_3 is E or W.
5. The compound of claim 1, wherein X_4 is V, I or Y.
6. The compound of claim 1, wherein X_5 is M or L.
7. The compound of claim 1, wherein X_6 is W, Y or F.
8. The compound of claim 1, wherein X_7 is M, Y or D.
9. The compound of claim 1, wherein X_8 is C or M.
10. The compound of claim 1, wherein the sequence of amino acids is selected from the group consisting of:

CAGEVMHMCC (SEQ ID NO: 8);
CNREIEAMCC (SEQ ID NO: 9);
CADEVMHFCC (SEQ ID NO: 10);
CNREIMWMCC (SEQ ID NO: 11);
CSHEVWWYCC (SEQ ID NO: 12);
CSREVLYYCC (SEQ ID NO: 13);
CFIEGPWVCC (SEQ ID NO: 14);
CFVEGNWYCC (SEQ ID NO: 15);
CAAEVMVNCC (SEQ ID NO: 16);
CSDEVIFYCC (SEQ ID NO: 17);
CDREIMWFCC (SEQ ID NO: 18);

Exhibit A: Complete set of the claims, as filed.

CAHEVMWMCC (SEQ ID NO: 19);
CGSEVTFMCC (SEQ ID NO: 20);
CLEEIMWLCC (SEQ ID NO: 21);
CAREVLAMCC (SEQ ID NO: 22);
CSVEVMQMCC (SEQ ID NO: 23);
CTNVQLMHYC (SEQ ID NO: 24);
CDVWQLFDRC (SEQ ID NO: 25);
CSFVQLNSIC (SEQ ID NO: 26);
CDYWQWFDKC (SEQ ID NO: 27);
CESFWVELWC (SEQ ID NO: 28);
CVPWMFYDLC (SEQ ID NO: 29);
CDPWMFYDLC (SEQ ID NO: 30);
CDPWVLFDEC (SEQ ID NO: 31);
CDHWTYFDMC (SEQ ID NO: 32);
CVVWTLYDKC (SEQ ID NO: 33);
CPDWYQSYMC (SEQ ID NO: 34);
CPDWYSYYMC (SEQ ID NO: 35);
CPEWYTDVMC (SEQ ID NO: 36);
CPDWYLDYMC (SEQ ID NO: 37);
CPEWYLDYMC (SEQ ID NO: 38);
CPDWYLPYMC (SEQ ID NO: 39);
CPEWYLPYMC (SEQ ID NO: 40);
CQDWWVELWC (SEQ ID NO: 41);
CPDWYLPWMC (SEQ ID NO: 42);
CACMLRVVHC (SEQ ID NO: 43);
CQRAGYMLAC (SEQ ID NO: 44);
CHANPVWGEC (SEQ ID NO: 45);
CFWSDWGQTC (SEQ ID NO: 46);
CPHWTSYYMC (SEQ ID NO: 47);
CETLCGACFC (SEQ ID NO: 48);
CATTINDTLC (SEQ ID NO: 49);

Exhibit A: Complete set of the claims, as filed.

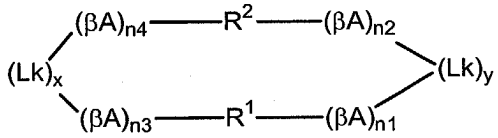
CLNYPHPVFC (SEQ ID NO: 50);
CMDGEMAVDC (SEQ ID NO: 51);
CNMGWMSWPC (SEQ ID NO: 52);
CETYADWLGC (SEQ ID NO: 53);
CDPWMFFDMC (SEQ ID NO: 54);
CDPWIWYDLC (SEQ ID NO: 55);
CDPWIMYDRC (SEQ ID NO: 56);
CDPWVFFDIC (SEQ ID NO: 57);
CDPWTYYDLC (SEQ ID NO: 58);
CDPWIFYDRC (SEQ ID NO: 59);
CDPWLFYDLC (SEQ ID NO: 60);
CDPWVWYDLC (SEQ ID NO: 61);
CDPWIFFDRC (SEQ ID NO: 62);
CDPWMFFDQC (SEQ ID NO: 63);
CDPWLWYDRC (SEQ ID NO: 64);
CDVWVWYDQC (SEQ ID NO: 65);
CDPWIYYDLC (SEQ ID NO: 66);
CVPWTLFDLC (SEQ ID NO: 67);
CPAWYLEYMC (SEQ ID NO: 68);
CPDWYLEYMC (SEQ ID NO: 69);
CKYWQWFDKC (SEQ ID NO: 70); and
CDHWMWYDKC (SEQ ID NO: 71).

11. The compound of claim 10, wherein the sequence of amino acids is selected from the group consisting of:

GCNREIEAMCCG (SEQ ID NO: 72);
GCPEWYTDVMCG (SEQ ID NO: 73);
NWYCMDGEMAVDCEAT (SEQ ID NO: 74);
WQSCNMGWMSWPCYFV (SEQ ID NO: 75);
HELCETYADWLGCVEW (SEQ ID NO: 76);
PCDPWMFFDMCERW (SEQ ID NO: 77);
LRGCDPWIWYDLCPAV (SEQ ID NO: 78);

GYLCDPWIXYDRCLGF (SEQ ID NO: 79);
RFACDPWVFFDICGYW (SEQ ID NO: 80);
GYWCDPWTYYDLCLTA (SEQ ID NO: 81);
MWTCDPWIFYDRCFLN (SEQ ID NO: 82);
GSSCDPWLFYDLCLLD (SEQ ID NO: 83);
GGGCDPWVWYDLCWCD (SEQ ID NO: 84);
YTSCDPWIFFDRCMSV (SEQ ID NO: 85);
DPYCDPWMFFDQCAYL (SEQ ID NO: 86);
REFCDPWLWYDRCL (SEQ ID NO: 87);
NTGCDVWVWYDQCFAM (SEQ ID NO: 88);
LVFCDPWIYYDLCMDT (SEQ ID NO: 89);
GCSFVQLNSICG (SEQ ID NO: 90);
GCPAWYLEYMCG (SEQ ID NO: 91);
GCPDWYLEYMCG (SEQ ID NO: 92);
GCKYWQWFDKCG (SEQ ID NO: 93); and
GCDHWMWYDKCG (SEQ ID NO: 94).

12. The compound of claim 1, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of formula (I); βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a C_{1-12} linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

13. The compound of claim 1, containing a disulfide bond.

14. The compound of claim 1, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

15. The compound of claim 1, wherein the N-terminus of the peptide is acetylated.

16. The compound of claim 1, wherein the C-terminus of the peptide is amidated.

17. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 1 in combination with a pharmaceutically acceptable carrier.

18. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 10-40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids having the structural formula (I)

(I) $CX_1X_2X_3X_4X_5X_6X_7X_8C$ (SEQ ID NO: 1)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X_1 is A, N, S, F, D, G, L, T, E, V, P, Q, H, M or K; X_2 is M, G, R, H, D, I, V, A, S, E, N, F, Y, P, C, W or T; X_3 is E, V, W, F, M, A, N, S, L, T, Y, G or P; X_4 is V, I, G, Q, W, M, T, Y, L, P, D, C, E or A; X_5 is M, E, W, L, P, N, I, T, V, F, Y, Q, S, R, W, G, H or D; X_6 is H, A, W, Y, V, F, Q, M, N, E, S, D, P or G; X_7 is M, F, Y, V, N, L, H, D, S, W, G, Q, C or T; and X_8 is C, Y, R, I, K, W, L, E, M, H, A, T, F, D, P, G or Q.

19. The method of claim 18, wherein the G-CSF modulator is an agonist for the G-CSFR.

20. The method of claim 19, wherein the patient suffers from a depressed neutrophil count.

21. The method of claim 20, wherein the depressed neutrophil count is caused by a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

22. The method of claim 18, wherein the G-CSF modulator is an antagonist for the G-CSFR.

23. A compound comprising a peptide chain approximately 9 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (II)

(II) $X^I_1X^I_2X^I_3SGWVWX^I_4$ (SEQ ID NO: 2)

wherein each amino acid is indicated by the standard one-letter abbreviation, and wherein X^I_1 is S, Q, R, L or Y; X^I_2 is N, S, T, A or D; X^I_3 is E, D or N; and X^I_4 is L V, T, P or H.

24. The compound of claim 23, wherein X^I_1 is S or Q.

25. The compound of claim 23, wherein X^I_2 is S.

26. The compound of claim 23, wherein X^I_3 is N.

27. The compound of claim 23, wherein X^I_4 is V.

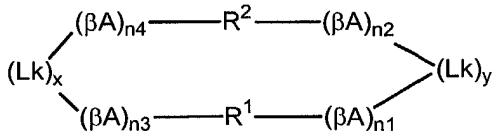
28. The compound of claim 23, wherein the sequence of amino acids is selected from the group consisting of:

SNESGWVWL (SEQ ID NO: 95);
QSNSGWVWV (SEQ ID NO: 96);
RTESGWVWT (SEQ ID NO: 97);
RANSGWVWV (SEQ ID NO: 98);
YDNSGWVWH (SEQ ID NO: 99); and
LSDSGWVWVP (SEQ ID NO: 100).

29. The compound of claim 28, wherein the sequence of amino acids is selected from the group consisting of:

EQSNSGWVWVGGGGC (SEQ ID NO: 101);
CEQSNSGWVWV (SEQ ID NO: 102);
EQSNSGWVWVGGGGCKKK (SEQ ID NO: 103);
EQSNSGWVWVGKKKC (SEQ ID NO: 104);
EQSNSGWVWVGKKK (SEQ ID NO: 105);
KKKEQSNSGWVWV (SEQ ID NO: 106);
EQSNSGWVWVGKKKSKKK (SEQ ID NO: 107);
EQSNSGWVWVGGCKKK (SEQ ID NO: 108);
EQSNSGWVWVGGGGGGCKKK (SEQ ID NO: 109);
SNESGWVWLP (SEQ ID NO: 110);
EQSNSGWVWV (SEQ ID NO: 111);
SRTESGWVWT (SEQ ID NO: 112);
QRANSGWVWV (SEQ ID NO: 113);
DYDNSGWVWH (SEQ ID NO: 114).
EQSNSGWVWVGKKKK (SEQ ID NO: 115);
EQSNSGWVWVGGGGSKKK (SEQ ID NO: 116);
EQSNSGWVWVGGGGS (SEQ ID NO: 117);
EQSNSGWVWVGGGGSEQSNSGWVWVGGGGS (SEQ ID NO: 118);
RYQSFELSDSGWVWVPVARH (SEQ ID NO: 119); and
EQSNSGWVWVGGGGCKKKC (SEQ ID NO: 492)

30. The compound of claim 23, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of formula (II); βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a $C_{1\text{-}12}$ linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

31. The compound of claim 30, wherein the dimer is:

NH_2-EQSNSGWVWVGGGGC-$CONH_2$ (SEQ ID NO: 101)
|
NH_2-EQSNSGWVWVGGGGC-$CONH_2$ (SEQ ID NO: 101).

32. The compound of claim 23, containing a disulfide bond.

33. The compound of claim 23, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

34. The compound of claim 23, wherein the N-terminus of the peptide is acetylated.

35. The compound of claim 23, wherein the C-terminus of the peptide is amidated.

36. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 23 in combination with a pharmaceutically acceptable carrier.

37. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 9 to 40 amino acids that binds to G-CSF and contains a sequence of amino acids having the structural formula (II)

(II) $X^I_1X^I_2X^I_3$SGWVWX^I_4 (SEQ ID NO: 2)

wherein each amino acid is indicated by the standard one-letter abbreviation, and wherein X^I_1 is S, Q, R, L or Y; X^I_2 is N, S, T, A or D; X^I_3 is E, D or N; and X^I_4 is L V, T, P or H.

38. The method of claim 37, wherein the G-CSF modulator is an agonist for the G-CSFR.

39. The method of claim 38, wherein the patient suffers from a depressed neutrophil count.

40. The method of claim 39, wherein the depressed neutrophil count is caused by a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

41. The method of claim 37, wherein the G-CSF modulator is an antagonist for the G-CSFR.

42. A compound comprising a peptide chain approximately 6 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (III)

(III) $ERX^{II}_1X^{II}_2X^{II}_3C$ (SEQ ID NO: 3)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^{II}_1 is D, L, S, G, E, A, K or Y; X^{II}_2 is W, Y, F, L or V; and X^{II}_3 is F, G, M or L.

43. The compound of claim 42, wherein X^{II}_1 is D or L.

44. The compound of claim 42, wherein X^{II}_2 is W.

45. The compound of claim 42, wherein X^{II}_3 is F.

46. The compound of claim 42, wherein the sequence of amino acids is selected from the group consisting of:

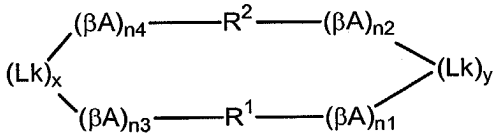
ERDWFC (SEQ ID NO: 120);
ERDWGC (SEQ ID NO: 121);
ERLWFC (SEQ ID NO: 122);
ERSYFC (SEQ ID NO: 123);
ERGWFC (SEQ ID NO: 124);
EREWFC (SEQ ID NO: 125);
ERAWFC (SEQ ID NO: 126);
ERLYFC (SEQ ID NO: 127);
ERYFMC (SEQ ID NO: 128);
ERLFLC (SEQ ID NO: 129);
ERALMC (SEQ ID NO: 130);
ERDVMC (SEQ ID NO: 131); and
ERKWFC (SEQ ID NO: 132).

47. The compound of claim 46, wherein the sequence of amino acids is selected from the group consisting of:

ETWGERDWFC (SEQ ID NO: 133);
ETWGERDWGC (SEQ ID NO: 134);

STAERLWFCG (SEQ ID NO: 135);
YETAERSYFC (SEQ ID NO: 136);
ADNAERGWFC (SEQ ID NO: 137);
QSNSEREWFC (SEQ ID NO: 138);
STSERAWFCG (SEQ ID NO: 139);
ASWSERGWFC (SEQ ID NO: 140);
ELSSEREWFC (SEQ ID NO: 141);
DMQGERGWFC (SEQ ID NO: 142);
SSSERAWFCG (SEQ ID NO: 143);
GNMRERLYFC (SEQ ID NO: 144);
QPNRERYFMC (SEQ ID NO: 145);
SVTRERLFLC (SEQ ID NO: 146);
IPLSERALMCSSWNC (SEQ ID NO: 147);
WARSERDVMCLSYVC (SEQ ID NO: 148);
QSNSEREWFCG (SEQ ID NO: 149);
QSNSEREWFCGGGGS (SEQ ID NO: 150);
NLEEALAQERLWFCRSGNC (SEQ ID NO: 151); and
NLESYEMEERKWFCKMFSC (SEQ ID NO: 152).

48. The compound of claim 42, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of formula (III); βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a C_{1-12} linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

49. The compound of claim 42, containing a disulfide bond.

50. The compound of claim 49, selected from the group consisting of:

NH_2-STAERLWFCG-$CONH_2$ (SEQ ID NO: 135)
|
NH_2-STAERLWFCG-$CONH_2$ (SEQ ID NO: 135);

NH_2-QSNSEREWFC-$CONH_2$ (SEQ ID NO: 138)
|
NH_2-QSNSEREWFC-$CONH_2$ (SEQ ID NO: 138); and

NH_2-QSNSEREWFCG-$CONH_2$ (SEQ ID NO: 149)
|
NH_2-QSNSEREWFCG-$CONH_2$ (SEQ ID NO: 149).

51. The compound of claim 42, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

52. The compound of claim 42, wherein the N-terminus of the peptide is acetylated.

53. The compound of claim 42, wherein the C-terminus of the peptide is amidated.

54. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 42 in combination with a pharmaceutically acceptable carrier.

55. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 6 to 40 amino acids that binds to G-CSFR and contains a sequence of amino acids having the structural formula (III)

(III) $ERX^{II}_1X^{II}_2X^{II}_3C$ (SEQ ID NO: 3)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^{II}_1 is D, L, S, G, E, A, K or Y; X^{II}_2 is W, Y, F, L or V; and X^{II}_3 is F, G, M or L.

56. The method of claim 55, wherein the G-CSF modulator is an agonist for the G-CSFR.

57. The method of claim 56, wherein the patient suffers from a depressed neutrophil count.

58. The method of claim 57, wherein the depressed neutrophil count is caused by a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

59. The method of claim 55, wherein the G-CSF modulator is an antagonist for the G-CSFR.

60. A compound comprising a peptide chain approximately 9 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (IV)

(IV) $X^{III}_1MVYX^{III}_2X^{III}_3PX^{III}_4W$ (SEQ ID NO: 4)

wherein each amino acid in indicated by standard one-letter abbreviation, and wherein X^{III}_1 is D or E; X^{III}_2 is A or T; X^{III}_3 is Y or V; and X^{III}_4 is P or Y.

61. The compound of claim 60, wherein the sequence of amino acids is selected from the group consisting of:

DMVYAYPPW (SEQ ID NO: 153); and

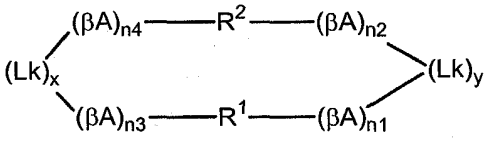
EMVYTVPYW (SEQ ID NO: 154).

62. The compound of claim 61, wherein the sequence of amino acids is selected from the group consisting of:

DMVYAYPPWS (SEQ ID NO: 155); and

DEMVYTVPYW (SEQ ID NO: 156).

63. The compound of claim 60, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of formula (IV); βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a $C_{1\text{-}12}$ linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

64. The compound of claim 60, containing a disulfide bond.

65. The compound of claim 60, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

66. The compound of claim 60, wherein the N-terminus of the peptide is acetylated.

67. The compound of claim 60, wherein the C-terminus of the peptide is amidated.

68. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 60 in combination with a pharmaceutically acceptable carrier.

Exhibit A: Complete set of the claims, as filed.

69. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 9 to 40 amino acids that binds to G-CSFR and contains a sequence of amino acids having the structural formula (IV)

(IV) $X^{III}_1MVYX^{III}_2X^{III}_3PX^{III}_4W$ (SEQ ID NO: 4)

wherein each amino acid in indicated by standard one-letter abbreviation, and wherein X^{III}_1 is D or E; X^{III}_2 is A or T; X^{III}_3 is Y or V; and X^{III}_4 is P or Y.

70. The method of claim 69, wherein the G-CSF modulator is an agonist for the G-CSFR.

71. The method of claim 70, wherein the patient suffers from a depressed neutrophil count.

72. The method of claim 71, wherein the depressed neutrophil count is caused by a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

73. The method of claim 69, wherein the G-CSF modulator is an antagonist for the G-CSFR.

74. A compound comprising a peptide chain approximately 12 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (V)

(V) $CX^{IV}_1X^{IV}_2X^{IV}_3X^{IV}_4X^{IV}_5X^{IV}_6X^{IV}_7X^{IV}_8X^{IV}_9X^{IV}_{10}C$ (SEQ ID NO: 5)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^{IV}_1 is E, G, P, N, R, T, W, S, L, H, A, Q or Y; X^{IV}_2 is S, T, E, A, D, G, W, P, L, N, V, Y, R or M; X^{IV}_3 is R, Y, V, Q, E, T, L, P, S, K, M, A or W; X^{IV}_4 is L, M, G, F, W, R, S, V, P, A, D, C or T; X^{IV}_5 is V, T, A, R, S, L, W, C, I, E, P, H, F, D or Q; X^{IV}_6 is E, Y, G, T, Q, M, S, N, A or P; X^{IV}_7 is C, V, D, G, L, W, E, V, I, S, M or A; X^{IV}_8 is S, Y, A, W, P, V, L, Q, G, K, F, I, E or D; X^{IV}_9 is R, W, M, D, H, V, G, A, Q, L, S, E or Y; X^{IV}_{10} is M, L, I, S, V, P, W, F, T, Y, R, or Q.

75. The compound of claim 74, wherein X^{IV}_1 is E.

76. The compound of claim 74, wherein X^{IV}_2 is S or A.

77. The compound of claim 74, wherein X^{IV}_3 is R.

78. The compound of claim 74, wherein X^{IV}_4 is L.

79. The compound of claim 74, wherein X^{IV}_5 is V or S.

80. The compound of claim 74, wherein X^{IV}_6 is E.

81. The compound of claim 74, wherein X^{IV}_7 is C.

82. The compound of claim 74, wherein X^{IV}_8 is S.

83. The compound of claim 74, wherein X^{IV}_9 is R.

84. The compound of claim 74, wherein X^{IV}_{10} is L.

85. The compound of claim 74, wherein the sequence of amino acids is selected from the group consisting of:

CESRLVECSRMC (SEQ ID NO: 157);
CETYMTYVYWLC (SEQ ID NO: 158);
CGERLAECARLC (SEQ ID NO: 159);
CESRLRECSMLC (SEQ ID NO: 160);
CEARLSECSRIC (SEQ ID NO: 161);
CPARLLECSRMC (SEQ ID NO: 162);
CESVGVGDWWSC (SEQ ID NO: 163);
CEDRLVEGPWVC (SEQ ID NO: 164);
CNDQFRTCVDVC (SEQ ID NO: 165);
CRGEWWELYHPC (SEQ ID NO: 166);
CEDTRTGWAWSC (SEQ ID NO: 167);
CTWLSSGELVWC (SEQ ID NO: 168);
CWPPVCEVSGIC (SEQ ID NO: 169);
CSLSPIQLQHLC (SEQ ID NO: 170);
CLARLEECSRFC (SEQ ID NO: 171);
CHNSSPMVGVTC (SEQ ID NO: 172);
CHVSPVQIKALC (SEQ ID NO: 173);
CAAPATSWFQYC (SEQ ID NO: 174);
CASKLHECSLRC (SEQ ID NO: 175);
CEPMDSNGIVQC (SEQ ID NO: 176);
CQYASAADEQRC (SEQ ID NO: 177);
CEYWDEPSLSWC (SEQ ID NO: 178);
CERECFQMLERC (SEQ ID NO: 179);
CGMSTDELDEIC (SEQ ID NO: 180);
CYVSPSTGLYSC (SEQ ID NO: 181);
CEARLVECSRLC (SEQ ID NO: 182);
CESRLSECSRMC (SEQ ID NO: 183);

CELKLQECARRC (SEQ ID NO: 184);

CELKLQEAARRC (SEQ ID NO: 185); and

CLERLEECSRFC (SEQ ID NO: 186).

86. The compound of claim 85, wherein the sequence of amino acid is selected from the group consisting of:

GGCESRLVECSRMC (SEQ ID NO: 187);

GGCETYMTYVYWLC (SEQ ID NO: 188);

EWLCESVGVGDWWSC (SEQ ID NO: 189);

YHPCEDRLVEGPWVCCRS (SEQ ID NO: 190);

WLLCNDQFRTCVDVCDNV (SEQ ID NO: 191);

IAECRGEWWELYHPCLAA (SEQ ID NO: 192);

TWYCEDTRTGWAWSCLEL (SEQ ID NO: 193);

QLDCTWLSSGELVWCSDW (SEQ ID NO: 194);

QFDCTWLSSGELVWCSDW (SEQ ID NO: 195);

CWPPVCEVSGICS (SEQ ID NO: 196);

CGCSLSPIQLQHLC (SEQ ID NO: 197);

CGCHVSPVQIKALC (SEQ ID NO: 198);

GCHVSPVQIKALC (SEQ ID NO: 199);

GTSCAAPATSWFQYCVLP (SEQ ID NO: 200);

RMDCASKLHECSLRCAYA (SEQ ID NO: 201);

GVVCEPMDSNGIVQCSMR (SEQ ID NO: 202);

IDVCQYASAADEQRCLRI (SEQ ID NO: 203);

NVLCEYWDEPSLSWCLSS (SEQ ID NO: 204);

CQCERECFQMLERC (SEQ ID NO: 205);

FCSCGMSTDELDEICAIW (SEQ ID NO: 206);

EEVCYVSPSTGLYSCYDQ (SEQ ID NO: 207);

LLDICELKLQECARRCN (SEQ ID NO: 208);

GGGLLDICELKLQECARRCN (SEQ ID NO: 209);

GRTGGGLLDICELKLQECARRCN (SEQ ID NO: 210);

LGIEGRTGGGLLDICELKLQECARRCN (SEQ ID NO: 211);

LLDICELKLQEAARRCN (SEQ ID NO: 212); and

KLLDICELKLQEAARRCN (SEQ ID NO: 213).

87. The compound of claim 86, wherein the sequence of amino acids is selected from the group consisting of:

LLDICELKLQECARRCN (SEQ ID NO: 208);

GGGLLDICELKLQECARRCN (SEQ ID NO: 209);

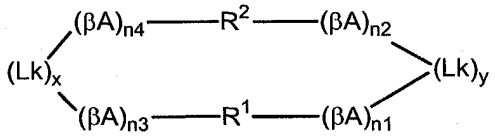
GRTGGGLLDICELKLQECARRCN (SEQ ID NO: 210);

LGIEGRTGGGLLDICELKLQECARRCN (SEQ ID NO: 211);

LLDICELKLQEAARRCN (SEQ ID NO: 212); and

KLLDICELKLQEAARRCN (SEQ ID NO: 213).

88. The compound of claim 74, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of formula (V); βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a C_{1-12} linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

89. The compound of claim 74, containing a disulfide bond.

90. The compound of claim 89, having the structure:

NH_3^+-LLDICELKLQECARRCN-COO^- (SEQ ID NO: 208)
|
NH_3^+-LLDICELKLQECARRCN-COO^- (SEQ ID NO: 208).

91. The compound of claim 74, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

92. The compound of claim 74, wherein the N-terminus of the peptide is acetylated.

93. The compound of claim 74, wherein the C-terminus of the peptide is amidated.

94. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 74 in combination with a pharmaceutically acceptable carrier.

95. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 12 to 40 amino acids that binds to G-CSFR and contains a sequence of amino acids having the structural formula (V)

(V) $CX^{IV}_1X^{IV}_2X^{IV}_3X^{IV}_4X^{IV}_5X^{IV}_6X^{IV}_7X^{IV}_8X^{IV}_9X^{IV}_{10}C$ (SEQ ID NO: 5)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^{IV}_1 is E, G, P, N, R, T, W, S, L, H, A, Q or Y; X^{IV}_2 is S, T, E, A, D, G, W, P, L, N, V, Y, R or M; X^{IV}_3 is R, Y, V, Q, E, T, L, P, S, K, M, A or W; X^{IV}_4 is L, M, G, F, W, R, S, V, P, A, D, C or T; X^{IV}_5 is V, T, A, R, S, L, W, C, I, E, P, H, F, D or Q; X^{IV}_6 is E, Y, G, T, Q, M, S, N, A or P; X^{IV}_7 is C, V, D, G, L, W, E, V, I, S, M or A; X^{IV}_8 is S, Y, A, W, P, V, L, Q, G, K, F, I, E or D; X^{IV}_9 is R, W, M, D, H, V, G, A, Q, L, S, E or Y; X^{IV}_{10} is M, L, I, S, V, P, W, F, T, Y, R, or Q.

96. The method of claim 95, wherein the G-CSF modulator is an agonist for the G-CSFR.

97. The method of claim 96, wherein the patient suffers from a depressed neutrophil count.

98. The method of claim 97, wherein the depressed neutrophil count is caused by a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

99. The method of claim 95, wherein the G-CSF modulator is an antagonist for the G-CSFR.

100. The method of claim 99, wherein the G-CSF modulator is

NH_3^+-LLDICELKLQECARRCN-COO^- (SEQ ID NO: 208)
| | | |
NH_3^+-LLDICELKLQECARRCN-COO^- (SEQ ID NO: 208).

101. A compound comprising a peptide chain approximately 9 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (VI)

(VI) $X^V_1X^V_2X^V_3X^V_4X^V_5X^V_6CX^V_7X^V_8$ (SEQ ID NO: 6)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^V_1 is E, C, Q, V, or Y; X^V_2 is E, A, L, M, S, W, or Q; X^V_3 is K, R or T; X^V_4 is L, A, or V; X^V_5 is R, A, M, H, E, V, L, G, D, Q, or S; X^V_6 is E or V; X^V_7 is A or G; X^V_8 is R, H, G or L.

102. The compound of claim 101, wherein X^V_1 is E.

103. The compound of claim 101, wherein X^V_2 is A or L.

104. The compound of claim 101, wherein X^V_3 is K or R.

105. The compound of claim 101, wherein X^V_4 is L.

106. The compound of claim 101, wherein X^V_6 is E.

107. The compound of claim 101, wherein X^V_7 is A.

108. The compound of claim 101, wherein X^V_8 is R.

109. The compound of claim 101, wherein the sequence of amino acids is selected from the group consisting of:

EEKLRECAR (SEQ ID NO: 214);
EARLAECAR (SEQ ID NO: 215);
CMKLMECAR (SEQ ID NO: 216);
ELRLRECAH (SEQ ID NO: 217);
EAKLHECAR (SEQ ID NO: 218);
ELKLAECAR (SEQ ID NO: 219);
EARLEECAR (SEQ ID NO: 220);
EAKLRECAR (SEQ ID NO: 221);
ELRLAECAR (SEQ ID NO: 222);
ESRLAECAR (SEQ ID NO: 223);
EAKLVECAR (SEQ ID NO: 224);
ESRLRECAR (SEQ ID NO: 225);
EAKLAECAR (SEQ ID NO: 226);
QWRLEECAR (SEQ ID NO: 227);
QLRLEECAR (SEQ ID NO: 228);
ELRLEECAR (SEQ ID NO: 229);
EAKLLECAR (SEQ ID NO: 230);
EARAGVCAG (SEQ ID NO: 231);
EAKAGVCAG (SEQ ID NO: 232);
VARLEECAR (SEQ ID NO: 233);
ELKLDECAR (SEQ ID NO: 234);
EWRLQECAR (SEQ ID NO: 235);
EAKLSECAR (SEQ ID NO: 236);
EARLSECAR (SEQ ID NO: 237);
ELKLLECAR (SEQ ID NO: 238);

ELRLQECGR (SEQ ID NO: 239);
EQKLAECAR (SEQ ID NO: 240);
ELRLQECAR (SEQ ID NO: 241);
ELKLEECAR (SEQ ID NO: 242);
ESRLEECAR (SEQ ID NO: 243);
EATVQECAR (SEQ ID NO: 244);
ELKLQECAR (SEQ ID NO: 245);
YSRLEECGR (SEQ ID NO: 246);
ELRLRECAL (SEQ ID NO: 247);
EARLLECAR (SEQ ID NO: 248);
ESRLLECAR (SEQ ID NO: 249);
VLKLEECAR (SEQ ID NO: 250);
ESKLAECAR (SEQ ID NO: 251);
ESKLRECAR (SEQ ID NO: 252);
EYKLGECAR (SEQ ID NO: 253);
ESRLQECAR (SEQ ID NO: 254);
QARLAECAR (SEQ ID NO: 255);
ELKKQECAR (SEQ ID NO: 256);
ESRLSECAR (SEQ ID NO: 257);
EARLEECGR (SEQ ID NO: 258);
ESRLAECGR (SEQ ID NO: 259);
EWRLEECAR (SEQ ID NO: 260);
EARLSECGR (SEQ ID NO: 261);
AARLAECAR (SEQ ID NO: 262);
EWKLAECAR (SEQ ID NO: 263);
ESKLEECAR (SEQ ID NO: 264);
DVKLAECAR (SEQ ID NO: 265);
ELQLEECAR (SEQ ID NO: 266); and
EYKLASCAR (SEQ ID NO: 267).

110. The compound of claim 109, wherein the sequence of amino acids is selected from the group consisting of:

RLSICEEKLRECARGC (SEQ ID NO: 268);
PLTTCEARLAECARQL (SEQ ID NO: 269);
LALCMKLMECARRY (SEQ ID NO: 270);
ELVMCELRLRECAHRA (SEQ ID NO: 271);
PLARCEAKLHECARQL (SEQ ID NO: 272);
LLSVCELKLAECARSK (SEQ ID NO: 273);
RLEWCEARLEECARRC (SEQ ID NO: 274);
RLRVVEAKLRECARGR (SEQ ID NO: 275);
CVAHLELRLAECARQI (SEQ ID NO: 276);
HLARCESRLAECARQL (SEQ ID NO: 277);
RLALLEAKLVECARRL (SEQ ID NO: 278);
DLFSLESRLRECARRV (SEQ ID NO: 279);
AVPVLEAKLAECARRF (SEQ ID NO: 280);
YLQQLQWRLEECARGM (SEQ ID NO: 281);
YLELCQLRLEECARQFN (SEQ ID NO: 282);
ELHICELRLEECARGR (SEQ ID NO: 283);
RVARCELRLAECARKS (SEQ ID NO: 284);
YLEVLESRLAECARWK (SEQ ID NO: 285);
EAKLLECARAR (SEQ ID NO: 286);
ELSLCEARAGVCAGSVTK (SEQ ID NO: 287);
ELSLCEAKAGVCAGSVTK (SEQ ID NO: 288);
ALWQCVARLEECARSR (SEQ ID NO: 289);
CLKSCELKLDECARRM (SEQ ID NO: 290);
ALQTCEWRLQECARSR (SEQ ID NO: 291);
YISQCEAKLAECARLY (SEQ ID NO: 292);
ELSSCEAKLSECARRW (SEQ ID NO: 293);
ELSSCEARLSECARRW (SEQ ID NO: 294);
QLLQCELKLLECARQG (SEQ ID NO: 295);
ELLRCEARLAECARGC (SEQ ID NO: 296);
QLRQCELRLQECGRHGN (SEQ ID NO: 297);
PLTSCEQKLAECARRF (SEQ ID NO: 298);

LLGMCELRLQECARAK (SEQ ID NO: 299);
ELSRCELKLEECARGM (SEQ ID NO: 300);
DCRPCESRLEECARRL (SEQ ID NO: 301);
RLSVCEARLEECARQL (SEQ ID NO: 302);
PLKMCEATVQECARLI (SEQ ID NO: 303);
LLLFCEARLSECARHV (SEQ ID NO: 304);
SLSMCEARLAECARLL (SEQ ID NO: 305);
PLFSCELKLQECARRCN (SEQ ID NO: 306);
SLERCYSRLEECGRRI (SEQ ID NO: 307);
PLTSCELRLRECALRSN (SEQ ID NO: 308);
KLAACELKLAECARRW (SEQ ID NO: 309);
KLAACELRLAECARRW (SEQ ID NO: 310);
ALTRCELRLAECARKI (SEQ ID NO: 311);
LLQQCELKLAECARSI (SEQ ID NO: 312);
QLWQCEARLLECARRS (SEQ ID NO: 313);
RLRLCESRLLECARSL (SEQ ID NO: 314);
QLETCVLKLEECARRCN (SEQ ID NO: 315);
ALSQCELRLAECARSVTK (SEQ ID NO: 316);
ELKLAECARRS (SEQ ID NO: 317);
ALSRCESKLAECARRQ (SEQ ID NO: 318);
LMSTCESKLRECARSL (SEQ ID NO: 319);
SLQRCEYKLGECARSL (SEQ ID NO: 320);
RLELLESRLQECARQLN (SEQ ID NO: 321);
QMEWCQARLAECARCCN (SEQ ID NO: 322);
PLFSCELKKQECARRCN (SEQ ID NO: 323);
LLDKCESRLSECARRL (SEQ ID NO: 324);
LLARCEARLEECGRQC (SEQ ID NO: 325);
DLLYCESRLAECGRM (SEQ ID NO: 326);
ALQMCEWRLEECARRL (SEQ ID NO: 327);
LLTMCEARLSECGRRL (SEQ ID NO: 328);
ALWRCESRLAECARRS (SEQ ID NO: 329);

LLATCAARLAECARQL (SEQ ID NO: 330);

LQTCEWKLAECARSN (SEQ ID NO: 331);

PLRSCESKLEECARQL (SEQ ID NO: 332);

CLRALDVKLAECARHL (SEQ ID NO: 333);

RLKTLELQLEECARRS (SEQ ID NO: 334);

KLRDVELKLAECARRS (SEQ ID NO: 335);

SLQRCEYKLASCARSL (SEQ ID NO: 336);

RLARCELRLAECARKS (SEQ ID NO: 337);

DLWYLESKLEECARRCN (SEQ ID NO: 338);

DLWYLESKLEECARRANG (SEQ ID NO: 339);

DLWYLESKLEECARRCNG (SEQ ID NO: 340);

KQRELELKLAECARRS (SEQ ID NO: 341);

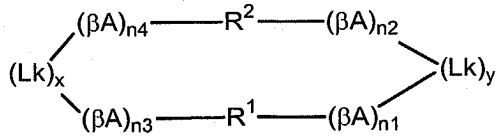
QMQEWCARLAECARCCN (SEQ ID NO: 342); and

LLDICELKLQECARRAN (SEQ ID NO: 343).

111. The compound of claim 110, wherein the sequence is:

LLDICELKLQECARRAN (SEQ ID NO: 343).

112. The compound of claim 101, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of formula (V); βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a C_{1-12} linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

113. The compound of claim 101, containing a disulfide bond.

114. The compound of claim 113, selected from the group consisting of:

[H]-DLWYLESKLEECARRANG-[NH_2] (SEQ ID NO: 339)
|
[H]-DLWYLESKLEECARRANG-[NH_2] (SEQ ID NO: 339);

[H]-DLWYLESKLEECARRCNG -[NH_2] (SEQ ID NO: 340); and
|____|

[H]-LLDICELKLQECARRAN-[OH] (SEQ ID NO: 343).
|_____|

115. The compound of claim 101, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

116. The compound of claim 101, wherein the N-terminus of the peptide is acetylated.

117. The compound of claim 101, wherein the C-terminus of the peptide is amidated.

118. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 101 in combination with a pharmaceutically acceptable carrier.

119. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 9 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (VI)

(VI) $X^V_1X^V_2X^V_3X^V_4X^V_5X^V_6CX^V_7X^V_8$ (SEQ ID NO: 6)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^V_1 is E, C, Q, V, or Y; X^V_2 is E, A, L, M, S, W, or Q; X^V_3 is K, R or T; X^V_4 is L, A, or V; X^V_5 is R, A, M, H, E, V, L, G, D, Q, or S; X^V_6 is E or V; X^V_7 is A or G; X^V_8 is R, H, G or L.

120. The method of claim 119, wherein the G-CSF modulator is an agonist for the G-CSFR.

121. The method of claim 120, wherein the patient suffers from a depressed neutrophil count.

122. The method of claim 121, wherein the depressed neutrophil count is caused a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

123. The method of claim 119, wherein the G-CSF modulator is an antagonist for the G-CSFR.

124. A compound comprising a peptide chain approximately 10 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (VII)

(VII) $X^{VI}_1X^{VI}_2X^{VI}_3X^{VI}_4X^{VI}_5EX^{VI}_6X^{VI}_7X^{VI}_8X^{VI}_9$ (SEQ ID NO: 7)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^{VI}_1 is A, E or G; X^{VI}_2 is E, H or D; X^{VI}_3 is R or G; X^{VI}_4 is K, Y, M, N, Q, R, D, I, S or E; X^{VI}_5 is A, S or P; X^{VI}_6 is E, D, T, Q, K or A: X^{VI}_7 is R, W, K, L, S, A or Q; X^{VI}_8 is R or E; and X^{VI}_9 is W, G, or R.

125. The compound of claim 124, wherein X^{VI}_1 is A.

126. The compound of claim 124, wherein X^{VI}_2 is E.

127. The compound of claim 124, wherein X^{VI}_3 is R.

128. The compound of claim 124, wherein X^{VI}_5 is A.

129. The compound of claim 124, wherein X^{VI}_6 is E.

130. The compound of claim 124, wherein X^{VI}_7 is R.

131. The compound of claim 124, wherein X^{VI}_8 is R.

132. The compound of claim 124, wherein and X^{VI}_9 is W.

133. The compound of claim 124, wherein the sequence of amino acids is selected from the group consisting of:

AERKAEERRW (SEQ ID NO: 344);
AERYAEEREG (SEQ ID NO: 345);
AERMAEERRW (SEQ ID NO: 346);
AERKAEERRR (SEQ ID NO: 347);
AHRNAEERRW (SEQ ID NO: 348);
AERKSEDWRW (SEQ ID NO: 349);
AERKAEEKRR (SEQ ID NO: 350);
AERQAETRRW (SEQ ID NO: 351);
AERNAEERRW (SEQ ID NO: 352);
AERQAEERRW (SEQ ID NO: 353);
AERRAEERRW (SEQ ID NO: 354);
AERDAEQRRW (SEQ ID NO: 355);
AERIAEERRW (SEQ ID NO: 356);
AERSAEERRW (SEQ ID NO: 357);

AERKAEELRW (SEQ ID NO: 358);
AERKAEESRW (SEQ ID NO: 359);
EERKAEERRW (SEQ ID NO: 360);
ADGKAEERRW (SEQ ID NO: 361);
ADGKAEELRW (SEQ ID NO: 362);
ADGMPEERRW (SEQ ID NO: 363);
ADGEAEKRRW (SEQ ID NO: 364);
ADGNAEERRW (SEQ ID NO: 365);
ADGEAEKARW (SEQ ID NO: 366);
AEGEAEKARW (SEQ ID NO: 367);
GERKAEERRW (SEQ ID NO: 368);
AEREAEERRW (SEQ ID NO: 369);
ADGEAEARRW (SEQ ID NO: 370);
ADGRAEEARW (SEQ ID NO: 371);
AEGRAEEARW (SEQ ID NO: 372);
AEREAEKARW (SEQ ID NO: 373);
AERKAEEQRW (SEQ ID NO: 374);
AERDAEKRRW (SEQ ID NO: 375); and
AEREAEKLRW (SEQ ID NO: 376).

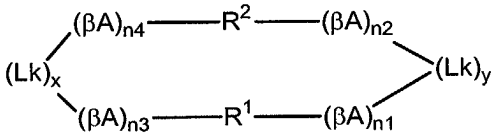
134. The compound of claim 133, wherein the sequence of amino acids is selected from the group consisting of:

MLAERKAEERRWFNTHGRE (SEQ ID NO: 377);
MLAERKAEERRWFNTHGREK (SEQ ID NO: 378);
GGGMLAERKAEERRWFNTHGRE (SEQ ID NO: 379);
CMLAERKAEERRWFNTHGRE (SEQ ID NO: 380);
CMLAERKAEERRWFNTHGREK (SEQ ID NO: 381);
MLAERYAEEREGFNMQWRE (SEQ ID NO: 382);
MLAERMAEERRWFRRMG (SEQ ID NO: 383);
IVAERKAEERRRLNTEGHE (SEQ ID NO: 384);
ILAHRNAEERRWFQKHGR (SEQ ID NO: 385);
MLAERKSEDWRWLKTHGRD (SEQ ID NO: 386);

MLAERKAEEKRRLKTQGRE (SEQ ID NO: 387);
ILAERQAETRRWMRNAGSVTK (SEQ ID NO: 388);
MLAERNAEERRWLKRQCG (SEQ ID NO: 389);
MLAERQAEERRWLKMHGGE (SEQ ID NO: 390);
MLAERRAEERRWLKTQGGD (SEQ ID NO: 391);
MLAERQAEERRWLKTQGRD (SEQ ID NO: 392);
MLAERKAEERRWFKTHGRE (SEQ ID NO: 393);
MLAERKAEERRWFNNQGRE (SEQ ID NO: 394);
MPAERDAEQRRWLKTHGRE (SEQ ID NO: 395);
ILAERIAEERRWLKTQGR (SEQ ID NO: 396);
MLAERKAEERRWLQTHGRE (SEQ ID NO: 397);
ILAERSAEERRWLKTQGRE (SEQ ID NO: 398);
LLAERKAEELRWLKTHGRE (SEQ ID NO: 399);
MLAERKAEERRWLQTHGRE (SEQ ID NO: 400);
MLAERNAEERRW (SEQ ID NO: 401);
MFAERKAEESRWLQSQGRE (SEQ ID NO: 402);
MLEERKAEERRWLKTHGR (SEQ ID NO: 403);
MLAERKAEERRWLKMQGRE (SEQ ID NO: 404);
MLAERNAEERRWFYTHGRE (SEQ ID NO: 405);
MLADGKAEERRWLKTHGLD (SEQ ID NO: 406);
MIADGKAEERRWLKTHGRD (SEQ ID NO: 407);
MLADGKAEELRWLKTQGSD (SEQ ID NO: 408);
MLAERNAEERRWLKTHGRD (SEQ ID NO: 409);
MLADGKAEELRWLKTQGRE (SEQ ID NO: 410);
ILADGKAEERRWLKTHGRD (SEQ ID NO: 411);
MLADGMPEERRWLQTHGRD (SEQ ID NO: 412);
MLADGEAEKRRWLNTHGRD (SEQ ID NO: 413);
MLADGNAEERRWLMTHGRD (SEQ ID NO: 414);
MLADGEAEKARWLKTQGRE (SEQ ID NO: 415);
MLAEGEAEKARWLKTQGRE (SEQ ID NO: 416);
MLADGKAEERRWLKTQGRE (SEQ ID NO: 417);

MLAERKAEERRWLSAHVRE (SEQ ID NO: 418);
LLGERKAEERRWYKTHARE (SEQ ID NO: 419);
MLAERKAEERRWLMTHGHD (SEQ ID NO: 420);
MLAERKAEERRWLKSQCLE (SEQ ID NO: 421);
LLAEREAEERRWFKTHGRE (SEQ ID NO: 422);
MLADGEAEARRWFNMHGRE (SEQ ID NO: 423);
MLADGRAEEARWLKTQGSE (SEQ ID NO: 424);
MLAEGRAEEARWLKTQGSE (SEQ ID NO: 425);
MLAEREAEKARWLKTQGRE (SEQ ID NO: 426);
MMAERKAEEQRWFDIHGRD (SEQ ID NO: 427);
LTAERDAEKRRWLLTHGGE (SEQ ID NO: 428);
MLAERQAEERRWLKSQRGE (SEQ ID NO: 429);
LLAERKAEERRWFATHGRD (SEQ ID NO: 430);
MLAEREAEKLRWLKSQERA (SEQ ID NO: 431);
MLAERKAEERRWLKTHGGE (SEQ ID NO: 432);
KGGGMLAERKAEERRWFNTHGRE (SEQ ID NO: 490); and
KSTGGLTAERDAEKRRWLLTHGGE (SEQ ID NO: 491).

135. The compound of claim 124, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of formula (VI); βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a C_{1-12} linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

136. The compound of claim 135, wherein the dimer is selected from the group consisting of:

MLAERKAEERRWFNTHGRE (SEQ ID NO: 377)
\
MLAERKAEERRWFNTHGRE-K(NH_2) (SEQ ID NO: 378) and

CMLAERKAEERRWFNTHGRE (SEQ ID NO: 380)
|\
CMLAERKAEERRWFNTHGRE-K (SEQ ID NO: 381).

137. The compound of claim 124, containing a disulfide bond.

138. The compound of claim 124, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

139. The compound of claim 124, wherein the N-terminus of the peptide is acetylated.

140. The compound of claim 124, wherein the C-terminus of the peptide is amidated.

141. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 124 in combination with a pharmaceutically acceptable carrier.

142. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 10 to 40 amino acids in length that binds to G-CSFR and contains a sequence of amino acids of formula (VII)

(VII) $X^{VI}_1X^{VI}_2X^{VI}_3X^{VI}_4X^{VI}_5EX^{VI}_6X^{VI}_7X^{VI}_8X^{VI}_9$ (SEQ ID NO: 7)

wherein each amino acid is indicated by standard one-letter abbreviation, and wherein X^{VI}_1 is A, E or G; X^{VI}_2 is E, H or D; X^{VI}_3 is R or G; X^{VI}_4 is K, Y, M, N, Q, R, D, I, S or E; X^{VI}_5 is A, S or P; X^{VI}_6 is E, D, T, Q, K or A: X^{VI}_7 is R, W, K, L, S, A or Q; X^{VI}_8 is R or E; and X^{VI}_9 is W, G, or R.

143. The method of claim 142, wherein the G-CSF modulator is an agonist for the G-CSFR.

144. The method of claim 143, wherein the patient suffers from a depressed neutrophil count.

145. The method of claim 144, wherein the depressed neutrophil count is caused a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

146. The method of claim 142, wherein the G-CSF modulator is an antagonist for the G-CSFR.

147. A compound comprising a peptide chain approximately 6 to 40 amino acids in length that binds to G-CSF and contains a sequence of amino acids selected from the group consisting of:

CTWTDLESVY (SEQ ID NO: 433);
HTTNEQFFMC (SEQ ID NO: 434);
DTWLELESRY (SEQ ID NO: 435);
HNSSPMVGVT (SEQ ID NO: 436);
DWQKTIPAYW (SEQ ID NO: 437);
RWGREGLVAALL (SEQ ID NO: 438);
WSGTRVWRCVVT (SEQ ID NO: 439);
MSLLSYLRS (SEQ ID NO: 440);
LDLLAI (SEQ ID NO: 441);
RIYGVK (SEQ ID NO: 442);
MIWHMFMSLLF (SEQ ID NO: 443);
FFWASWMHLLW (SEQ ID NO: 444);
FDDCWREREQFLFQAL (SEQ ID NO: 445);
CGRASECFRLLEM (SEQ ID NO: 446);
RECFQMLER (SEQ ID NO: 447);
CSIRWDFVPGYGLC (SEQ ID NO: 448);
WMQCWDSLSLCYDM (SEQ ID NO: 449);
ALLMCESKLAECARAR (SEQ ID NO: 450);
LAHCKKRKEECAAG (SEQ ID NO: 451);
SIDGVYLRTSRT (SEQ ID NO: 452);
SIDGVYLRTRSRTRY (SEQ ID NO: 453);
VWRLRGSTLRGLRD (SEQ ID NO: 454);
DRGGGTVGVYWWESY (SEQ ID NO: 455);
VWGTVGTWLEY (SEQ ID NO: 456);
LMWVSAY (SEQ ID NO: 457);
RASDEYGALVRFCTNL (SEQ ID NO: 458);
NYWCDSNWVCEIA (SEQ ID NO: 459);
LAHCLLRLEECAAG (SEQ ID NO: 460);

LALCLARLRECAGG (SEQ ID NO: 461);

CESRLVECSRM (SEQ ID NO: 462);

LLDIAELKLQECARRCN (SEQ ID NO: 463);

KLLDIAELKLQECCARRCN (SEQ ID NO: 464);

CSTGGGLTAERDAEKRRWLLTHGGE (SEQ ID NO: 465)

LTAERDAEKRRWLLTHGGEGG (SEQ ID NO: 466);

LTAERDAEKRRWLLTHGGEGGK (SEQ ID NO: 467);

LTAERDAEKRRWLLTHGGEGGGGG (SEQ ID NO: 468);

LTAERDAEKRRWLLTHGGEGGGGGK (SEQ ID NO: 469);

ESGWVW (SEQ ID NO: 470);

NSGWVW (SEQ ID NO: 471);

SGWVW (SEQ ID NO: 472);

PLGKCEATCREMARYFN (SEQ ID NO: 473);

SLQRCEYKLASVRGLCN (SEQ ID NO: 474)

DLWYLESKLEEAARRCNG (SEQ ID NO: 475);

PYMGTRSRAKLLRQQ (SEQ ID NO: 476):

RNAGERRWFKTQGWY (SEQ ID NO: 477):

MLAERNADDRRWFNTHGRD (SEQ ID NO: 478):

MMADGRLRNSVGLILWCD (SEQ ID NO: 479);

MLADGRLRNVVG (SEQ ID NO: 480);

LLADVRRRNGVGLLRMGRD (SEQ ID NO: 481);

MLADGRLRNFGG (SEQ ID NO: 482);

TYMTYVYWLC (SEQ ID NO: 483); (CORE 158)

RFGERWGL (SEQ ID NO: 484);

HWLWWGWNF (SEQ ID NO: 485);

RECFQMLERC (SEQ ID NO: 486);

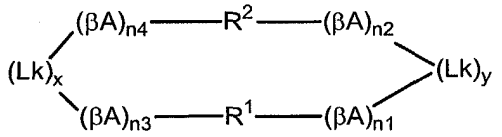
ILAHRNAKERRWFQKHGR (SEQ ID NO: 487); and

CSTGGGLTAERDAEKRRWLLTHGGEK (SEQ ID NO: 489).

148. The compound of claim 147, wherein the sequence is selected from the group consisting of:

LLDIAELKLQECARRCN (SEQ ID NO: 463); and
KLLDIAELKLQECCARRCN (SEQ ID NO: 464).

149. The compound of claim 147, comprising a dimer having the structure of formula (VIII)



(VIII)

wherein R^1 and R^2 are independently selected from the sequences of amino acids of claim 122; βA is a β-alanine residue; n1, n2, n3, n4, x and y are independently zero or one with the proviso that the sum of x and y is either one or two; and Lk is a terminal linking moiety selected from the group consisting of a disulfide bond, a carbonyl moiety, a C_{1-12} linking moiety optionally terminated with one or two -NH- linkages and optionally substituted at one or more available carbon atoms with a lower alkyl substituent, a lysine residue or a lysine amide.

150. The compound of claim 149, wherein the dimer is selected from the group consisting of:

CSTGGGLTAERDAEKRRWLLTHGGE (SEQ ID NO: 465)
|
CSTGGGLTAERDAEKRRWLLTHGGE (SEQ ID NO: 489);

LTAERDAEKRRWLLTHGGEGG (SEQ ID NO: 466)
|
LTAERDAEKRRWLLTHGGEGG-K (SEQ ID NO: 467); and

LTAERDAEKRRWLLTHGGEGGGGG (SEQ ID NO: 468)
|
LTAERDAEKRRWLLTHGGEGGGGG-K (SEQ ID NO: 469).

151. The compound of claim 147, containing a disulfide bond.

152. The compound of claim 151, selected from the group consisting of:

[H]-DLWYLESKLEEAARRCNG -[NH_2] (SEQ ID NO: 475)
|
[H]-DLWYLESKLEEAARRCNG-[NH_2] (SEQ ID NO: 475);

[H]-LLDIAELKLQECARRCN-[OH] (SEQ ID NO: 463); and
|_____|

[H]-KLLDIAELKLQECARRCN-[OH] (SEQ ID NO: 464).
|_____|

153. The compound of claim 147, wherein the N-terminus of the peptide is coupled to a polyethylene glycol molecule.

154. The compound of claim 147, wherein the N-terminus of the peptide is acetylated.

155. The compound of claim 147, wherein the C-terminus of the peptide is amidated.

156. A pharmaceutical composition comprising a therapeutically effective amount of the compound of claim 147 in combination with a pharmaceutically acceptable carrier.

157. A method for treating a patient who would benefit from administration of a G-CSF modulator, comprising administering to the patient a therapeutically effective amount of a compound comprising a peptide chain approximately 6 to 40 amino acids in length that binds to G-CSF and contains a sequence of amino acids selected from the group consisting of:

CTWTDLESVY (SEQ ID NO: 433);
HTTNEQFFMC (SEQ ID NO: 434);
DTWLELESRY (SEQ ID NO: 435);
HNSSPMVGVT (SEQ ID NO: 436);
DWQKTIPAYW (SEQ ID NO: 437);
RWGREGLVAALL (SEQ ID NO: 438);
WSGTRVWRCVVT (SEQ ID NO: 439);
MSLLSYLRS (SEQ ID NO: 440);
LDLLAI (SEQ ID NO: 441);
RIYGVK (SEQ ID NO: 442);
MIWHMFMSLLF (SEQ ID NO: 443);

FFWASWMHLLW (SEQ ID NO: 444);
FDDCWREREQFLFQAL (SEQ ID NO: 445);
CGRASECFRLLEM (SEQ ID NO: 446);
RECFQMLER (SEQ ID NO: 447);
CSIRWDFVPGYGLC (SEQ ID NO: 448);
WMQCWDSLSLCYDM (SEQ ID NO: 449);
ALLMCESKLAECARAR (SEQ ID NO: 450);
LAHCKKRKEECAAG (SEQ ID NO: 451);
SIDGVYLRTSRT (SEQ ID NO: 452);
SIDGVYLRTRSRTRY (SEQ ID NO: 453);
VRWLRGSTLRGLRDR (SEQ ID NO: 454);
DRGGGTVGVYWWESY (SEQ ID NO: 455);
VWGTVGTWLEY (SEQ ID NO: 456);
LMWVSAY (SEQ ID NO: 457);
RASDEYGALVRFCTNL (SEQ ID NO: 458);
NYWCDSNWVCEIA (SEQ ID NO: 459);
LAHCLLRLEECAAG (SEQ ID NO: 460);
LALCLARLRECAGG (SEQ ID NO: 461);
CESRLVECSRM (SEQ ID NO: 462);
LLDIAELKLQECARRCN (SEQ ID NO: 463);
KLLDIAELKLQECCARRCN (SEQ ID NO: 464);
CSTGGGLTAERDAEKRRWLLTHGGE (SEQ ID NO: 465);
LTAERDAEKRRWLLTHGGEGG (SEQ ID NO: 466);
LTAERDAEKRRWLLTHGGEGGK (SEQ ID NO: 467);
LTAERDAEKRRWLLTHGGEGGGGG (SEQ ID NO: 468);
LTAERDAEKRRWLLTHGGEGGGGGK (SEQ ID NO: 469);
ESGWVW (SEQ ID NO: 470);
NSGWVW (SEQ ID NO: 471);
SGWVW (SEQ ID NO: 472);
PLGKCEATCREMARYFN (SEQ ID NO: 473);
SLQRCEYKLASVRGLCN (SEQ ID NO: 474);

DLWYLESKLEEAARRCNG (SEQ ID NO: 475);
PYMGTRSRAKLLRQQ (SEQ ID NO: 476);
RNAGERRWFKTQGWY (SEQ ID NO: 477);
MLAERNADDRRWFNTHGRD (SEQ ID NO: 478);
MMADGRLRNSVGLILWCD (SEQ ID NO: 479);
MLADGRLRNVVG (SEQ ID NO: 480);
LLADVRRRNGVGLLRMGRD (SEQ ID NO: 481);
MLADGRLRNFGG (SEQ ID NO: 482);
TYMTYVYWLC (SEQ ID NO: 483);
RFGERWGL (SEQ ID NO: 484);
HWLWWGWNF (SEQ ID NO: 485);
RECFQMLERC (SEQ ID NO: 486);
ILAHRNAKERRWFQKHGR (SEQ ID NO: 487); and
CSTGGGLTAERDAEKRRWLLTHGGEK (SEQ ID NO: 489).

158. The method of claim 157, wherein the G-CSF modulator is an agonist for the G-CSFR.

159. The method of claim 158, wherein the patient suffers from a depressed neutrophil count.

160. The method of claim 159, wherein the depressed neutrophil count is caused a condition selected from the group consisting of chemotherapy-induced neutropenia, AIDS-induced neutropenia and community-acquired pneumonia-induced neutropenia.

161. The method of claim 157, wherein the G-CSF modulator is an antagonist for the G-CSFR.